



## SEQUENCE LISTING

<110> University of Utah Research Foundation  
Yale University  
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Splawski, Igor  
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Goldstein, Steve A.N.

<120> MinK-Related Genes, Formation of Potassium Channels and  
Association with Cardiac Arrhythmia

<130> 2323-150.a

<140> 09/550,163

<141> 2000-04-14

<150> US 60/129,404

<151> 1999-04-15

<160> 22

<170> PatentIn version 3.1/2.0

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<222> (74)..(442)

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Asn Thr Thr Ala Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu
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Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe
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Gln Glu Lys Tyr Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala
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 agaattttca tggagattat gtgggtggcc aataaagata gatgacattt caatctcagt 622  
 gatttatgct tgcttggttg agcaatatat tgtgctgaag acctctttta ctttccgggc 682  
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 Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu Asn Phe Tyr Tyr  
 35 40 45  
 Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ser Phe Ile Ile  
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 Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser  
 65 70 75 80  
 Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Glu Lys Tyr  
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 Thr Gln Thr Leu Glu Asp Ala Phe Lys Lys Val Phe Ile Thr Tyr Met  
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gac agc tgg agg agg aac aca aca gcc gaa caa cag gcg ctc cag gcc 151  
 Asp Ser Trp Arg Arg Asn Thr Thr Ala Glu Gln Gln Ala Leu Gln Ala  
 25 30 35  
 aga gtg gat gcc gag aac ttc tac tac gtc atc ctg tac ctc atg gtg 199  
 Arg Val Asp Ala Glu Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val  
 40 45 50 55  
 atg atc ggc atg ttc gcc ttc atc gtg gtg gcc atc ctg gtg agc acg 247  
 Met Ile Gly Met Phe Ala Phe Ile Val Val Ala Ile Leu Val Ser Thr  
 60 65 70  
 gtg aag tcg aag cgg cgg gag cac tcc cag gac ccg tac cac cag tac 295  
 Val Lys Ser Lys Arg Arg Glu His Ser Gln Asp Pro Tyr His Gln Tyr  
 75 80 85  
 atc gtg gag gat tgg cag cag aag tat agg agt cag atc ttg cat ctg 343  
 Ile Val Glu Asp Trp Gln Gln Lys Tyr Arg Ser Gln Ile Leu His Leu  
 90 95 100  
 gaa gac tcc aag gcc acc atc cat gag aac ctg ggg gcg acg ggg ttc 391  
 Glu Asp Ser Lys Ala Thr Ile His Glu Asn Leu Gly Ala Thr Gly Phe  
 105 110 115  
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 Glu Gln Gln Ala Leu Gln Ala Arg Val Asp Ala Glu Asn Phe Tyr Tyr  
 35 40 45  
 Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ala Phe Ile Val  
 50 55 60  
 Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser  
 65 70 75 80  
 Gln Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Gln Lys Tyr  
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			20					25					30				
Pro	Gly	Pro	Gly	Leu	Gly	Pro	Asp	Asn	Gln	Thr	Glu	Glu	Arg	Arg	Ala		
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Ser	Leu	Pro	Gly	Arg	Asp	Asp	Asn	Ser	Tyr	Met	Tyr	Ile	Leu	Phe	Val		
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 aaggaactga ggggttgtgg gacatccacg aagagatcct caaagatgtc tcagagccag 180  
 cagagtctct gaactgtttg atcacattcc agctcttccc atacctcaat atctgttgct 240  
 atg gag act tcc aac ggg act gag acc tgg tac atg agc ctc cat gct 288  
 Met Glu Thr Ser Asn Gly Thr Glu Thr Trp Tyr Met Ser Leu His Ala  
 1 5 10 15  
 gtg ctg aag gct ctg aac acc acc ctt cac agt cac ttg ctc tgc cgg 336  
 Val Leu Lys Ala Leu Asn Thr Thr Leu His Ser His Leu Leu Cys Arg  
 20 25 30  
 cct ggg cca gga cca ggg cca gac aat caa act gag gat cgt cgg gct 384  
 Pro Gly Pro Gly Pro Gly Pro Asp Asn Gln Thr Glu Asp Arg Arg Ala  
 35 40 45  
 agc ctt cct ggt cgt aat gac aac tcc tac atg tat att ctc ttt gtc 432  
 Ser Leu Pro Gly Arg Asn Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val  
 50 55 60  
 atg ttc cta ttt gcc gtc act gtg ggc agt ctc atc ctg gga tat acc 480  
 Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr  
 65 70 75 80  
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 Arg Ser Arg Lys Val Asp Lys Arg Ser Asp Pro Tyr His Val Tyr Ile  
 85 90 95  
 aag aac cgt gtg tct atg atc tgatgtgagg aacctgaaga caatggaaga 579  
 Lys Asn Arg Val Ser Met Ile  
 100  
 ttacaatgtc tgaggattgt cttctggtgc ctccggaact caactcaacc atatcaagcc 639  
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gaagaggaag ctgtggcgaa gggaaatggg gcagaaagat gctctggata tataatcttt 879  
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                   20                  25                  30  
 Pro Gly Pro Gly Pro Gly Pro Asp Asn Gln Thr Glu Asp Arg Arg Ala  
                   35                  40                  45  
 Ser Leu Pro Gly Arg Asn Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val  
           50                  55                  60  
 Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr  
           65                  70                  75                  80  
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                   100

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 ttaaaatacg tttccagtt ttaaagatac tatttactgt atgctcctgt cttacattga 300  
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tca atg ctg aaa atg gag cct ctg aac agc acg cac ccc ggc acc gcc	648
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gcc tcc agc agc ccc ctg gag tcc cgt gcg gcc ggt ggc ggc agc gcc	696
Ala Ser Ser Ser Pro Leu Glu Ser Arg Ala Ala Gly Gly Gly Ser Gly	
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aat ggc aac gag tac ttc tac att ctg gtt gtc atg tcc ttc tac gcc	744
Asn Gly Asn Glu Tyr Phe Tyr Ile Leu Val Val Met Ser Phe Tyr Gly	
35 40 45	
att ttc ttg atc gga atc atg ctg ggc tac atg aaa tcc aag agg cgg	792
Ile Phe Leu Ile Gly Ile Met Leu Gly Tyr Met Lys Ser Lys Arg Arg	
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gag aag aag tcc agc ctc ctg ctg ctg tac aaa gac gag gag cgg ctc	840
Glu Lys Lys Ser Ser Leu Leu Leu Tyr Lys Asp Glu Glu Arg Leu	
65 70 75	
tgg ggg gag gcc atg aag ccg ctg ccc gtg gtg tcg ggc ctg agg tcg	888
Trp Gly Glu Ala Met Lys Pro Leu Pro Val Val Ser Gly Leu Arg Ser	
80 85 90 95	
gtg cag gtg ccc ctg atg ctg aac atg ctg cag gag agc gtg gcg ccc	936
Val Gln Val Pro Leu Met Leu Asn Met Leu Gln Glu Ser Val Ala Pro	
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gcg ctg tcc tgc acc ctc tgt tcc atg gaa ggg gac agc gtg agc tcc	984
Ala Leu Ser Cys Thr Leu Cys Ser Met Glu Gly Asp Ser Val Ser Ser	
115 120 125	
gag tcc tcc tcc ccg gac gtg cac ctc acc att cag gag gag ggg gca	1032
Glu Ser Ser Ser Pro Asp Val His Leu Thr Ile Gln Glu Glu Gly Ala	
130 135 140	
gac gat gag ctg gag gag acc tcg gag acg ccc ctc aac gag agc agc	1080
Asp Asp Glu Leu Glu Glu Thr Ser Glu Thr Pro Leu Asn Glu Ser Ser	
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 35 40 45  
 Phe Leu Ile Gly Ile Met Leu Gly Tyr Met Lys Ser Lys Arg Arg Glu  
 50 55 60  
 Lys Lys Ser Ser Leu Leu Leu Tyr Lys Asp Glu Glu Arg Leu Trp  
 65 70 75 80  
 Gly Glu Ala Met Lys Pro Leu Pro Val Val Ser Gly Leu Arg Ser Val  
 85 90 95  
 Gln Val Pro Leu Met Leu Asn Met Leu Gln Glu Ser Val Ala Pro Ala  
 100 105 110  
 Leu Ser Cys Thr Leu Cys Ser Met Glu Gly Asp Ser Val Ser Ser Glu  
 115 120 125  
 Ser Ser Ser Pro Asp Val His Leu Thr Ile Gln Glu Glu Gly Ala Asp  
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 Met Leu Arg Met Glu Pro Leu Asn Ser  
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aca tac ccc agc gct gca gcc tcc agc agc ccc ctc gag tcc cat gtg 160  
 Thr Tyr Pro Ser Ala Ala Ser Ser Ser Pro Leu Glu Ser His Val 25  
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cct agt aac agc agt ggt aat ggc aat gaa tac ttc tat att ttg gtc 208  
 Pro Ser Asn Ser Ser Gly Asn Gly Asn Glu Tyr Phe Tyr Ile Leu Val 40  
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gtt atg tcc ttc tat ggc gtt ttc ctg atc gga atc atg ctg ggc tac 256  
 Val Met Ser Phe Tyr Gly Val Phe Leu Ile Gly Ile Met Leu Gly Tyr 55  
 45 50

atg aaa tcc aag agg cgg gag aag aag tcc agc ctt ctg ctg ttg tac 304  
 Met Lys Ser Lys Arg Arg Glu Lys Lys Ser Ser Leu Leu Leu Leu Tyr 70  
 60 65

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 Lys Asp Glu Glu Arg Leu Trp Gly Glu Ala Met Lys Pro Leu Pro Met 85  
 75 80

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 90 95 100

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 Gln Glu Ser Val Ala Pro Ala Leu Ser Cys Thr Leu Cys Ser Met Glu 120  
 110 115

ggg gac agt gtg agc tcc gag tcc tcc tct cct gat gtg cac ctt ccc 496  
 Gly Asp Ser Val Ser Ser Glu Ser Ser Ser Pro Asp Val His Leu Pro 135  
 125 130

atc cag gag gag ggg gct gat gac gag ctg gag gag acc tcc gag acg 544  
 Ile Gln Glu Glu Gly Ala Asp Asp Glu Leu Glu Glu Thr Ser Glu Thr 150  
 140 145

cct ctc aac gac agc agt gaa ggc tct tcc gag aac atc cac cag aat 592  
 Pro Leu Asn Asp Ser Ser Glu Gly Ser Ser Glu Asn Ile His Gln Asn 165  
 155 160

tcc tagcaccac caggtgctag gaggtagctc cgtaagctac acttgacaga 645  
 Ser  
 170

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 aagcagaaaa ctccccaag gtcaagtttg cctctagtgc aaaaccttct taatttttat 2025  
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<213> Mus musculus

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 35 40 45

Phe Leu Ile Gly Ile Met Leu Gly Tyr Met Lys Ser Lys Arg Arg Glu  
 50 55 60

Lys Lys Ser Ser Leu Leu Leu Tyr Lys Asp Glu Glu Arg Leu Trp  
 65 70 75 80

11

Gly Glu Ala Met Lys Pro Leu Pro Met Met Ser Gly Leu Arg Ser Gly  
85 90  
Gln Val Pro Met Met Leu Asn Met Leu Gln Glu Ser Val Ala Pro Ala  
100 105 110  
Leu Ser Cys Thr Leu Cys Ser Met Glu Gly Asp Ser Val Ser Ser Glu  
115 120 125  
Ser Ser Ser Pro Asp Val His Leu Pro Ile Gln Glu Glu Gly Ala Asp  
130 135 140  
Asp Glu Leu Glu Glu Thr Ser Glu Thr Pro Leu Asn Asp Ser Ser Glu  
145 150 155 160  
Gly Ser Ser Glu Asn Ile His Gln Asn Ser  
165 170

<210> 13  
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<220>  
<223> Description of Artificial Sequence:PCR primer for  
mutation screening

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<210> 14  
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<210> 15  
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mutation screening

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mutation screening

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21

<210> 17

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for  
mutation screening

<400> 17

aatgttctct ttcacatcgc tg

22

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer for  
mutation screening

<400> 18

tgtctggacg tcagatgtta g

21

<210> 19

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HA residues for  
epitope mapping

<220>

<221> PEPTIDE

<222> (10)

<223> Xaa represents encoded stop codon.

<400> 19

Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Xaa
1				5					10

<210> 20

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:cmv residues  
for epitope-mapping

<220>

<221> PEPTIDE

<222> (15)

<223> Xaa represents encoded stop codon.

<400> 20

Ile Ser Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Xaa  
1 5 10 15

<210> 21

<211> 130

<212> PRT

<213> rattus norvegicus

<400> 3

Met Ala Leu Ser Asn Ser Thr Thr Val Leu Pro Phe Leu Ala Ser Leu  
1 5 10 15

Trp Gln Glu Thr Asp Glu Pro Gly Gly Asn Met Ser Ala Asp Leu Ala  
20 25 30

Arg Arg Ser Gln Leu Arg Asp Asp Ser Lys Leu Glu Ala Leu Tyr Ile  
35 40 45

Leu Met Val Leu Gly Phe Phe Gly Phe Phe Thr Leu Gly Ile Met Leu  
50 55 60

Ser Tyr Ile Arg Ser Lys Lys Leu Glu His Ser His Asp Pro Phe Asn  
65 70 75 80

Val Tyr Ile Glu Ser Asp Ala Trp Gln Glu Lys Gly Lys Ala Leu Phe  
85 90 95

Gln Ala Arg Val Leu Glu Ser Phe Arg Ala Cys Tyr Val Ile Glu Asn  
100 105 110

Gln Ala Ala Val Glu Gln Pro Ala Thr His Leu Pro Glu Leu Lys Pro  
115 120 125

Leu Ser  
130

<210> 22

<211> 129

<212> PRT

<213> homo sapiens

<400> 4

Met Ile Leu Ser Asn Thr Thr Ala Val Thr Pro Phe Leu Thr Lys Leu  
1 5 10 15

Trp Gln Glu Thr Val Gln Gln Gly Gly Asn Met Ser Gly Leu Ala Arg  
 20 25 30

Arg Ser Pro Arg Ser Gly Asp Gly Lys Leu Glu Ala Leu Tyr Val Leu  
 35 40 45

Met Val Leu Gly Phe Phe Gly Phe Phe Thr Leu Gly Ile Met Leu Ser  
 50 55 60

Tyr Ile Arg Ser Lys Lys Leu Glu His Ser Asn Asp Pro Phe Asn Val  
 65 70 75 80

Tyr Ile Glu Ser Asp Ala Trp Gln Glu Lys Asp Lys Ala Tyr Val Gln  
 85 90 95

Ala Arg Val Leu Glu Ser Tyr Arg Ser Cys Tyr Val Val Glu Asn His  
 100 105 110

Leu Ala Ile Glu Gln Pro Asn Thr His Leu Pro Glu Thr Lys Pro Ser  
 115 120 125

Pro